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Longterm survival in primary glioblastoma with versus without isocitrate dehydrogenase mutations

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Abstract: **PURPOSE:** The determinants of longterm survival in glioblastoma have remained largely obscure. Isocitrate dehydrogenase (IDH) 1 or 2 mutations are common in WHO grade II and III gliomas, but rare in primary glioblastomas, and associated with longer survival. **EXPERIMENTAL DESIGN:** We compared clinical and molecular characteristics of 69 patients with centrally confirmed glioblastoma and survival > 36 months (LTS-36), including 33 patients surviving > 60 months (LTS-60), with 257 patients surviving < 36 months. MGMT promoter methylation, 1p/19q codeletions, EGFR amplification, TP53 mutations and IDH1/2 mutations were determined by standard techniques. **RESULTS:** The rate of IDH1/2 mutations in LTS-36 patients was 34% (23/67 patients) as opposed to 4.3% in controls (11/257 patients). Longterm survivors with IDH1/2 -mutant glioblastomas were younger, had almost no EGFR amplifications, but exhibited more often 1p/19q codeletions and TP53 mutations than LTS patients with IDH1/2 wildtype glioblastomas. Longterm survivors with IDH1/2-wildtype showed no distinguishing features from other patients with IDH1/2-wildtype glioblastomas except a higher rate of MGMT promoter methylation. Similarly, among 11 patients with IDH1/2-mutant glioblastomas without longterm survival, the only difference to IDH1/2-mutant longterm survivors was less frequent MGMT promoter methylation. Compared with LTS-36 patients, LTS-60 patients had less frequently TP53 mutations and radiotherapy alone as initial treatment. **CONCLUSIONS:** IDH1/2 mutations define a subgroup of tumors of LTS patients that exhibit molecular characteristics of WHO grade II/III gliomas and secondary glioblastomas. Determinants of LTS with IDH1/2-wildtype glioblastomas, which exhibit typical molecular features of primary glioblastomas, beyond MGMT promoter methylation, remain to be identified.

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Longterm survival in primary glioblastoma **with versus without** isocitrate dehydrogenase mutations

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Translational Relevance

Although the prognosis of patients with primary glioblastoma is generally poor, a minority of patients achieve longterm survival beyond 36 months. We here report that the rate of *IDH1/2* mutations in such patients is 34% as opposed to 4.3% in controls and thus substantially increased. Molecular marker profiles of *IDH1/2*-mutant primary glioblastoma correspond to that of secondary glioblastomas which are typically *IDH1/2*-mutant, too. *IDH1/2*-wildtype glioblastoma patients with longterm survival exhibit no characteristic marker profile distinguishing them from ordinary *IDH1/2*-wildtype glioblastoma patients with poor outcome, suggesting that host-derived factors, e.g., immune responsiveness, contribute to longterm survival in such patients.

Abstract

Purpose:

The determinants of longterm survival in glioblastoma have remained largely obscure. Isocitrate dehydrogenase (*IDH*) 1 or 2 mutations are common in WHO grade II and III gliomas, but rare in primary glioblastomas, and associated with longer survival.

Experimental Design:

We compared clinical and molecular characteristics of 69 patients with centrally confirmed glioblastoma and survival > 36 months (LTS-36), including 33 patients surviving > 60 months (LTS-60), with 257 patients surviving < 36 months. *MGMT* promoter methylation, 1p/19q codeletions, *EGFR* amplification, *TP53* mutations and *IDH1/2* mutations were determined by standard techniques.

Results:

The rate of *IDH1/2* mutations in LTS-36 patients was 34% (23/67 patients) as opposed to 4.3% in controls (11/257 patients). Longterm survivors with *IDH1/2* - mutant glioblastomas were younger, had almost no *EGFR* amplifications, but exhibited more often 1p/19q codeletions and *TP53* mutations than LTS patients with *IDH1/2* wildtype glioblastomas. Longterm survivors with *IDH1/2*-wildtype showed no distinguishing features from other patients with *IDH1/2*-wildtype glioblastomas except a higher rate of *MGMT* promoter methylation. Similarly, among 11 patients with *IDH1/2*-mutant glioblastomas without longterm survival, the only difference to *IDH1/2*-mutant longterm survivors was less frequent *MGMT* promoter methylation. Compared

with LTS-36 patients, LTS-60 patients had less frequently *TP53* mutations and radiotherapy alone as initial treatment.

Conclusions:

IDH1/2 mutations define a subgroup of tumors of LTS patients that exhibit molecular characteristics of WHO grade II/III gliomas and secondary glioblastomas.

Determinants of LTS with *IDH1/2*-wildtype glioblastomas, which exhibit typical molecular features of primary glioblastomas, beyond *MGMT* promoter methylation, remain to be identified.

Introduction

According to the World Health Organization (WHO) classification of brain tumors, glioblastomas (WHO grade IV) are defined as malignant astrocytic tumors with necrosis or microvascular proliferation or both (1). They most commonly occur either *de novo* and are then referred to as primary glioblastomas. Less frequently, they develop by progression from lower grade gliomas and are then referred to as secondary glioblastomas. The overall prognosis of glioblastoma has remained poor. In a prospective study of 301 primary glioblastoma patients enrolled in the German Glioma Network (GGN), we observed a median overall survival (OS) of 12.5 months (2). However, a small fraction of patients survive for more than 36 months. We have previously arbitrarily defined these patients as longterm survivors (LTS) and clinically characterized these patients as being younger at diagnosis and having a good initial performance score. Molecularly, their tumors showed an increased rate of *MGMT* promoter hypermethylation (74%, versus 30-35% in the general glioblastoma population) (3).

More recently, mutations in the gene encoding cytosolic NADP⁺-dependent isocitrate dehydrogenase 1 (*IDH1*) were identified in a minority of glioblastoma patients. They are more common in younger patients with primary glioblastoma and in patients with secondary glioblastoma and associated with increased OS (4, 5). In contrast, *IDH1* mutations are detected in 60 to 90% of diffusely infiltrating gliomas of WHO grades II and III (6-12). *IDH1* mutations occur exclusively in codon 132 and around 93% are R132H alterations (7). Moreover, mutations in the gene encoding the mitochondrial NADP⁺-dependent *IDH2* were identified in around 3% of WHO grade II or III gliomas and secondary glioblastomas (7, 12). Thus, the differential distribution of *IDH1/2* mutations among gliomas provided strong support for the

differentiation of secondary from primary glioblastoma and helped to molecularly dissect primary glioblastoma into distinct molecular subgroups (2, 10). These considerations led us to reanalyze and expand our original cohort of LTS glioblastoma patients (3) to address the question to what extent *IDH1/2* mutations account for the LTS phenotype and to identify characteristic features of the *IDH1/2*-wildtype LTS phenotype.

Material and Methods

Patient recruitment and histology

Sixty-nine patients with primary glioblastoma and an OS of longer > 36 months were identified by the 8 clinical centers and 2 associated clinical centers of the German Glioma Network (GGN; www.gliomnetzwerk.de). To be eligible for this analysis, it was required that the first histological diagnosis was that of a glioblastoma according to the WHO classification of central nervous system tumors (1) confirmed by central pathology review at the Brain Tumour Reference Center of the German Society of Neuropathology and Neuroanatomy (DGNN). Clinical and part of the molecular data of 36 patients have been published previously, but were updated and complemented for *IDH1/2* mutation status for this report (3), data of 9 other patients have been included in another publication of the GGN (2). The study was approved by the local ethics committees at the GGN clinical centres and written informed consent was obtained from each patient. As a reference group, we used a cohort of 257 primary glioblastoma patients published previously, but excluded all patients who survived for more than 36 months (2).

DNA extraction and analysis for MGMT promoter methylation, 1p/19q co-deletion, EGFR amplification, and TP53 mutation

DNA was extracted by standard methods either from formalin-fixed paraffin-embedded tumor tissue or from unfixed frozen tumor tissue samples. *MGMT* promoter methylation analysis was carried out by methylation-specific PCR. *EGFR* gene dosage was determined by real-time PCR analysis. Losses on 1p and 19q were determined either by multiplex ligation-dependent probe amplification (MLPA) or by

loss of heterozygosity (LOH) analysis of five different microsatellite markers on each chromosomal arm. *TP53* mutations were determined by single strand conformation polymorphism (SSCP) analysis followed by direct sequencing. Details of the respective molecular methods have been reported elsewhere (2, 3, 13).

IDH1 and IDH2 mutation analysis

IDH1 codon 132 and *IDH2* codon 172 were analyzed by direct sequencing. In case of ambiguous results, the *IDH1* or *IDH2* sequences were amplified by a different set of primers (6, 7). In addition, 26 LTS patients that carried neither *IDH1* nor *IDH2* mutations in the respective codons were tested for *IDH1* codon 100 mutations (14).

Statistical analysis

Fisher's exact test or the χ^2 tests were used to compare the frequencies of molecular aberrations and clinical data in the longterm survivor group versus the control group. Overall survival (OS) was calculated from the date of first surgery for glioblastoma until the time of death or last follow-up examination. Survival curves were compared using the log-rank test. Progression-free survival (PFS) was determined from day of first surgery until tumor progression, death, or end of follow-up. Cox regression and multivariate logistic regression analyses were performed. Hazard ratios (HR) and odds ratios (OR) with 95% confidence intervals (95% CI) were determined. All analyses were performed using IBM SPSS Statistics Version 20.

Results

Patient characteristics

We identified 69 patients with a survival > 36 months with a median follow-up of 73 months (LTS-36 cohort). Of these patients, 33 patients were ascertained to have survived for 60 months (LTS-60). These two cohorts were compared to a cohort of 257 glioblastoma patients who survived for less than 36 months and had a median follow-up of 23.6 months. Demographic, clinical and molecular characteristics of these three cohorts are summarized in Table 1. Seventeen of 69 LTS-36 and 15 of 33 LTS-60 patients are alive. LTS-36 patients were younger than control patients ($p<0.001$), but there was no enrichment of young patients in the LTS-60 group relative to the entire LTS-36 group of patients. The relative frequency of glioblastomas with oligodendroglial component was increased in the LTS cohorts. Initial KPS was similar among groups. There were fewer temporal tumors in LTS-36 patients ($p=0.185$), but this difference was not significant, even if the analysis was restricted to the control cohort *versus* the LTS-60 cohort. LTS-36 patients had only slightly more often a gross total resection and slightly less often a biopsy than control patients ($p=0.379$). Compared with control patients, LTS-36 patients had more often two or more further surgical interventions ($p<0.001$), were more often reirradiated ($p=0.066$), and received one or two lines of salvage chemotherapy more often ($p<0.001$). First-line treatment after surgery was overall similar except that LTS-60 patients received more often radiotherapy (RT) plus chemotherapy than RT alone relative to the other groups (n.s.). PFS with the first therapeutic intervention was five-fold as long in LTS-36 patients compared with control patients. Seven patients in the LTS-60 cohort have not suffered progression: five are alive, one died of renal cell carcinoma and cause of death is unknown in the other patient.

Molecular markers

The results of molecular analyses are summarized in Table 1 and Figure 1. LTS-36 patients had more often *MGMT* promoter-methylated tumors than the control group ($p < 0.001$). 1p/19q codeletions were rare and not more common in LTS patients. *EGFR* amplification was less common in LTS-36 patients ($p = 0.037$). The relative frequencies of *TP53* mutations were similar in LTS-36 and control patients ($p = 0.203$). *IDH1* mutations were much more common in the LTS-36 cohort (32.8%; 22/67) than in the control cohort (9/248) ($p < 0.001$). Among LTS patients, an *IDH1* R132H mutation was identified in 20 patients, an *IDH1* R132S mutation in one patient and an R132C mutation in one patient. In the control group, 9 *IDH1* mutations were found, all of the R132H type. One *IDH2* mutation was identified in 65 LTS-36 patients and two *IDH2* mutations in the control cohort. Among the 33 LTS-60 patients, fewer patients had *TP53* mutations than in the entire LTS-36 cohort. We observed 13 patients in the LTS-60 cohort that had no salvage therapy, 6 with *IDH1/2*-mutant tumors and 7 with *IDH1/2*-wildtype tumors. The tumors of 6 patients with *IDH1/2* mutation (median age 39 years) were *MGMT* promoter-methylated and had no *EGFR* mutation. Six of 7 patients with *IDH1/2* wildtype tumors (median age 60 years) had *MGMT* promoter methylation and 4 of 6 patients had tumors without *EGFR* mutation.

Prognostic factors for LTS-36

Next we asked which factors influenced the likelihood to become a LTS-36 patient and performed a multivariate logistic regression analysis. We included age (≤ 50 vs. > 50), KPS (≥ 80 vs. < 80), extent of resection (total vs. no total) and four genetic

alterations (*MGMT* promoter methylation, *IDH1/2* mutation, *EGFR* amplification, *TP53* mutation) as main factors. The most important prognostic factors for surviving for at least 36 months were *MGMT* status, *IDH1/2* status and age (Table 2). Table 3 shows a comparison of control patients as well as LTS-36 and LTS-60 patients with *versus* without *IDH1/2*-mutant tumors.

IDH-mutant versus IDH-wildtype glioblastoma with LTS

LTS patients with *IDH1/2*-mutant tumors were younger ($p=0.001$), had more often frontal as opposed to temporal or parietal tumors ($p=0.013$), had more often an oligodendroglial component ($p=0.099$), and were treated with RT alone initially more often ($p=0.169$). The molecular profile of *IDH1/2*-mutant tumors of LTS-36 patients was characterized by a higher rate of *MGMT* promoter methylation ($p=0.307$), 1p/19q codeletions ($p=0.046$), and *TP53* mutations ($p=0.345$), and the absence of *EGFR* amplification ($p=0.001$). Individual profiles are provided in Supplementary Tables 1 and 2. Among patients with wildtype *IDH1/2* status, *MGMT* promoter methylation provided a HR for death of 0.47 (95% CI 0.22-1.0, $p=0.053$). Only two patients had *IDH1/2*-mutant tumors lacking *MGMT* promoter methylation. Conversely, wildtype *TP53* status conferred a risk reduction both in patients with *IDH1/2*-mutant (0.28, 95% CI 0.09-0.82, $p=0.020$) and *IDH1/2* wildtype (0.59, 95% CI 0.24-0.1.45, $p=0.250$) tumors. We also assessed survival probability by molecular marker status in glioblastoma patients surviving for at least 36 months (LTS-36 cohort). Figure 2 shows that, among the LTS-36 patients, *IDH1/2* status was prognostically irrelevant ($p=0.414$) whereas *MGMT* promoter methylation ($p=0.078$), wildtype *TP53* status ($p=0.015$) and absence of *EGFR* amplification ($p=0.106$), with descending magnitude of effect, were associated with increased survival. Figure 3 shows the relative

distribution of patients with combinations of *IDH1/2* mutation and *MGMT* promoter methylation among the three cohorts, control, LTS-36 and LTS-60 patients.

IDH1/2-mutant LTS versus IDH1/2-mutant non-LTS

Columns 2 and 4 of table 3 allow to compare 23 LTS-36 patients with *IDH1/2* mutations versus 11 patients with *IDH1/2* mutations who survived for less than 36 months. Their median survival was 12 months and thus similar to the median survival of the general non-LTS cohort (Table 1). Death from tumor progression was confirmed in all 11 patients. None of these tumors had an oligodendroglioma component. The only other remarkable difference between these two cohorts of patients with *IDH1/2*-mutant glioblastoma were the rates of *MGMT* promoter methylation: there were 17 methylated, four weakly methylated and only two unmethylated tumors in *IDH1/2*-mutant LTS, but four methylated, one weakly methylated and six unmethylated tumors in the *IDH1/2*-mutant control patients ($p=0.016$).

IDH1/2-wildtype LTS versus IDH1/2-wildtype non-LTS

Columns 3 and 5 of table 3 allow to compare 44 LTS-36 patients without *IDH1/2* mutations versus 229 patients without *IDH1/2* mutations who survived for less than 36 months. The major differences between these groups were (expectedly) a higher number of patients who were not treated at all after surgery among control patients and a strong enrichment of patients with *MGMT* promoter-methylation in the LTS group.

Discussion

The clinical and molecular determinants of extended survival in glioblastoma remain uncertain, but are currently being elucidated using various approaches. Using one of the largest patient populations ever reported, the present study defines *MGMT* status, *IDH1/2* status and age as the most important prognostic factors for surviving the diagnosis of primary glioblastoma for at least 36 months (Table 2). Most LTS patients showed a classical glioblastoma morphology, although there was an enrichment for glioblastoma with oligodendroglial component in the LTS patients, in particular in the LTS-60 group. This histological subtype was more common in *IDH1/2* mutant tumors (Table 3). In contrast, extent of resection was not different between control group and LTS-36 patients. Moreover, although fewer patients in the LTS-60 group received RT alone as initial treatment, no such difference was seen between LTS-36 and control patients, and the differences in salvage treatment are unlikely to account for LTS since one might well argue that patients with less aggressive tumors are more likely to be eligible for multiple salvage therapies.

We delineate two main cohorts of primary glioblastoma patients with extended survival beyond 36 months, patients with *IDH1/2* mutations and patients without *IDH1/2* mutations. Furthermore, *IDH1/2*-wildtype tumors with and without *MGMT* promoter methylation can be distinguished (Figure 3). *IDH1/2* mutations have been associated with overall better prognosis across all diffusely infiltrating malignant astrocytic entities (9, 10, 12, 15, 16) and their absence in elderly glioblastoma patients may explain in part why age is a negative prognostic factor in this disease (17). However, it has never been explored whether tumors with *IDH1/2* mutations are enriched in longterm survivors of glioblastomas. Importantly, the present study only included patients with primary glioblastoma, that is, there was no evidence of a prior

lower-grade lesion in any of these patients. We report a rate of *IDH1/2* mutations of 34.3% (23/67) in LTS-36 patients which was much higher than in the general population of glioblastoma patients (5-10%). The molecular profile of these LTS-36 patients with *IDH1/2*-mutant primary glioblastoma was characterized by an increased prevalence of *TP53* mutations and the absence of *EGFR* amplification (Table 3).

Although a less malignant precursor lesion escaped clinical detection in this group of patients, the pattern of molecular alterations in their tumors was typical of secondary glioblastoma (9). Accordingly, the concept of primary and secondary glioblastoma should probably be replaced by a molecular concept, e.g., of *IDH1/2*-mutant glioblastoma rather than by the absence or presence of a clinically recognized precursor lesion, because future therapeutic decision making is likely to be more commonly based on molecular profiles.

The biological consequences of *IDH1/2* mutations are currently being elucidated. Mutant *IDH1* proteins generate excessive amounts of 2-hydroxyglutarate (2HG) from α -ketoglutarate (18). 2HG is a competitive inhibitor of various α -ketoglutarate-dependent dioxygenases (19). Accordingly, increased 2HG levels are predicted to inhibit histone demethylases and TET hydroxylases, thereby preventing histone demethylation and increasing promoter methylation of multiple genes (19, 20), including *MGMT* promoter methylation, and explaining why *IDH1/2*-mutant gliomas commonly exhibit the glioma-CpG island methylator phenotype (G-CIMP) (21, 22).

Both LTS cohorts, patients with and without *IDH1/2* mutations, share an increased prevalence of *MGMT* promoter methylation. All patients received alkylating agent chemotherapy at least once in the course of disease. Accordingly, it is impossible to dissect a prognostic versus predictive impact of *MGMT* promoter methylation in this cohort. Since most *IDH1/2*-mutant tumors exhibit *MGMT* promoter methylation, an

independent association of *MGMT* promoter methylation with outcome cannot be assessed in this cohort. The frequent *MGMT* promoter methylation in *IDH1/2* mutant glioblastomas suggests that *MGMT* belongs to the G-CIMP gene set (23). This association may explain why *MGMT* promoter methylation in patients with anaplastic gliomas, tumors with a high frequency of *IDH1/2* mutations, confers a prognostic benefit independent of the therapy regime (24, 25). In contrast, *MGMT* promoter methylation retained an (almost significant) prognostic significance in patients with *IDH1/2* wildtype glioblastoma. The molecular mechanisms inducing *MGMT* promoter methylation in glioblastomas of such patients remain to be identified. The speculation that these tumors carry alterations in other genes involved in the same pathway as *IDH1/2* has not been substantiated so far and is unlikely, given their differential genomic and epigenomic profiles. We confirm a lower rate of *EGFR* amplification in the LTS-36 cohort (26), but this can now be linked to its virtual absence in patients with *IDH1/2*-mutant tumors. Interestingly, the *EGFR* amplification rate in *IDH1/2*-wildtype tumors was similar in LTS-36 patients (43.2%) and in the control cohort (45.5%). Somewhat surprisingly, among the LTS-36 patients, patients with *TP53* mutant tumors had an inferior outcome. This observation corresponds to a similar observation at longterm follow-up in low grade astrocytoma patients (27) and was more prominent in the *IDH1/2*-mutant LTS-36 patients. Altogether, the determinants of longterm survival in patients with *IDH1/2* wildtype glioblastomas, which exhibit the typical molecular phenotype of glioblastomas, beyond *MGMT* promoter methylation remain to be identified, and even the absence of both *IDH1/2* mutations and *MGMT* promoter methylation does not preclude longterm survival. Finally, since the report of a small, nine patient series in 2006 (28), the present study represents the only characterization of primary glioblastoma patients surviving for 5 years or more, and molecular data on such patients have never been reported before.

Given limitations of tissue availability, we were unable to explore whether the LTS phenotype in our cohort is linked to recently characterized gene expression or DNA methylation signatures (29-31). The first high-throughput approaches have indeed suggested links between LTS and decreased retinoic acid signaling (32), enhanced immune-related gene expression (33), or distinct DNA methylation profiles (34), but more studies with larger patient populations seem to be required to decide whether tumor rather than host factors are chiefly responsible for LTS.

Table 1. Summary of patient characteristics.

	Control group (OS < 36 months) n=257	LTS > 36 months n=69	LTS > 60 months n=33
Age at diagnosis			
Median (years)	62	49	49
Range (years)	(19-86)	(21-74)	(22-74)
Gender			
Male	158 (61.5%)	35 (50.7%)	19 (57.6%)
Female	99 (38.5%)	34 (49.3%)	14 (42.4%)
Histological subtype			
Glioblastoma	235 (91.4%)	60 (87.0%)	28 (84.8%)
Glioblastoma olig. comp.	5 (1.9%)	4 (5.8%)	4 (12.1%)
Gliosarcoma	7 (2.7%)	2 (2.9%)	1 (3.0%)
Giant cell glioblastoma	7 (2.7%)	3 (4.3%)	-
Glioblastoma with single giant cells	3 (1.2%)	-	-
Survival			
Median follow-up (months)	23.6	73.0	73.6
Median PFS (months, 95% CI)	6.0 (5.4-6.6)	31.7 (25.8-37.6)	45.9 (38.1-53.7)
Median OS (months, 95% CI)	10.6 (9.6-11.7)	60.2 (52.8-67.5)	83.0 (71.1-94.5)
Alive at last follow-up	4 (1.6 %)	17 (24.6%)	15 (45.5%)
KPS at diagnosis			
90-100	106 (41.9%)	27 (41.5%)	13 (41.9%)
70-80	119 (47.0%)	32 (49.2%)	16 (51.6%)
<70	28 (11.1%)	6 (9.2%)	2 (6.5%)
No data	4	4	2
Tumor location			
Frontal	59 (23.1%)	17 (24.6%)	8 (24.2%)
Temporal	72 (28.2%)	14 (20.3%)	6 (18.2%)
Parietal	31 (12.2%)	11 (15.9%)	6 (18.2%)
Occipital	12 (4.7%)	1 (1.4%)	-
Not localized to one site	60 (23.5%)	20 (29.0%)	9 (27.3%)
Multifocal	3 (1.2%)	1 (1.4%)	1 (3.0%)
Others	18 (7.1%)	5 (7.2%)	3 (9.1%)
No data	2	-	-
Surgery			
Gross total resection	104 (40.9%)	32 (49.2%)	16 (50.0%)
Subtotal resection (50-99%)	95 (37.4%)	21 (32.3%)	12 (37.5%)
Partial resection (<50%)	29 (11.4%)	8 (12.3%)	3 (9.4%)
Biopsy	26 (10.2%)	4 (6.2%)	1 (3.1%)
No data	3	4	1
First-line therapy			
RT alone	61 (24.1%)	19 (27.5%)	5 (15.2%)
RT plus TMZ	151 (58.8%)	37 (53.6%)	21 (63.6%)
RT plus nitrosourea	2 (0.8%)	11 (15.9%)	6 (18.2%)
RT plus PC	1 (0.4%)	-	-
TMZ alone	10 (3.9%)	-	-
Procarbazine plus lomustine alone	-	1 (1.4%)	-
Nitrosourea alone	1 (0.4%)	-	-
No therapy	30 (11.6%)	1 (1.4%)	1 (3.0%)

Salvage therapies			
Surgery (1)	53 (20.6%)	16 (23.2%)	7 (21.2%)
Surgery (2)	11 (4.3%)	8 (11.6%)	4 (12.1%)
Surgery (>2)	1 (0.4%)	5 (7.2%)	3 (9.1%)
RT (first)	4 (1.6%)	1 (1.4%)	1 (3.0%)
RT (reirradiation)	19 (7.4%)	10 (14.5%)	5 (15.2%)
Chemotherapy (1)	53 (20.6%)	20 (29.0%)	13 (39.4%)
Chemotherapy (2)	25 (9.7%)	11 (15.9%)	4 (12.1%)
Chemotherapy (3)	6 (2.3%)	5 (7.2%)	-
Chemotherapy (>3)	1 (0.4%)	4 (5.8%)	2 (6.1%)
Other medical therapies (1)	20 (7.8%)	7 (10.1%)	2 (6.1%)
Other medical therapies (>1)	4 (1.6%)	1 (1.4%)	-
Including every drug not classified as chemotherapy, e.g., bevacizumab and tyrosine kinase inhibitors			
None	145 (56.4%)	21 (30.4%)	8 (22.2%)
MGMT promoter methylation status (MSP)			
Methylated	85 (33.6%)	41 (60.3%)	22 (66.7%)
Weakly methylated	15 (5.9%)	16 (23.5%)	7 (21.2%)
Unmethylated	153 (60.5%)	11 (16.2%)	4 (12.1%)
No data	4	1	-
1p/19q codeletion			
Yes	20 (8.4%)	6 (9.7%)	2 (6.5%)
No	217 (91.6%)	56 (90.3%)	29 (93.5%)
No data	20	7	2
EGFR amplification			
Yes	109 (43.4%)	20 (29.4%)	7 (21.2%)
No	142 (56.6%)	48 (70.6%)	26 (78.8%)
No data	6	1	-
TP53 mutation			
Yes	37 (15.0%)	14 (21.5%)	4 (12.5%)
No	210 (85.0%)	51 (78.5%)	28 (87.5%)
No data	10	4	1
IDH1 mutation			
Yes	9 (3.6%)	22 (32.8%)	12 (36.4%)
No	239 (96.4%)	45 (67.2%)	21 (63.6%)
No data	9	2	-
IDH2 mutation			
Yes	2 (0.8%)	1 (1.5%)	1 (3.1%)
No	239 (99.2%)	64 (98.5%)	31 (96.9%)
No data	16	4	1

Table 2. Multivariate logistic regression model for LTS-36 vs. control group

	OR	95%-CI	P value
Age ≤ 50 vs. > 50 (ref.)	5.0	2.3 to 10.5	< 0.001
KPS ≥ 80 vs. < 80 (ref.)	1.5	0.6 to 3.6	0.359
Extent of resection total vs. no total (ref.)	1.1	0.5 to 2.2	0.806
IDH1/2 mutant vs. wildtype (ref.)	4.0	1.5 to 11.0	0.007
MGMT methylated vs. unmethylated (ref.)	6.5	2.9 to 14.4	< 0.001
EGFR not amplified vs. amplified (ref.)	1.4	0.6 to 3.0	0.409
TP53 mutant vs. wildtype (ref.)	1.0	0.4 to 2.6	0.954

Table 3. Comparison of control group, LTS-36 and LTS-60 patients: *IDH1/2* mutant versus *IDH1/2* wildtype

	Control group (OS < 36 months) <i>IDH1/2</i> mutant n=11	Control group (OS < 36 months) <i>IDH1/2</i> wildtype n=229	LTS-36 <i>IDH</i> mutant n=23	LTS-36 <i>IDH</i> wildtype n=44	LTS-60 <i>IDH</i> mutant n=13	LTS-60 <i>IDH</i> wildtype n=20
Age at diagnosis						
Median (years)	44	63	41	55	39	60
Range (years)	27-79	19-86	(22-71)	(21-74)	(22-54)	(32-74)
Gender						
Male	5 (45.5%)	141 (61.6%)	12 (52.2%)	23 (52.3%)	7 (53.8%)	12 (60.0%)
Female	6 (54.5%)	88 (38.4%)	11 (47.8%)	21 (47.7%)	6 (46.2%)	8 (40.0%)
Histological subtype						
Glioblastoma	9 (81.8%)	209 (91.3%)	20 (87.0%)	38 (86.4%)	10 (76.9%)	18 (90.0%)
Glioblastoma olig. comp.	-	5 (2.2%)	3 (13.0%)	1 (2.3%)	3 (23.1%)	1 (5.0%)
Gliosarcoma	-	7 (3.1%)	-	2 (4.5%)	-	1 (5.0%)
Giant cell glioblastoma	-	7 (3.1%)	-	3 (6.8%)	-	-
Glioblastoma with single giant cells	2 (18.2%)	1 (0.4%)				
Survival						
Median follow-up (months)	-	21.1	73.9	73.0	73.9	73.6
MedianPFS (months, 95% CI)	6.8 (3.0-10.5)	6.0 (5.4-6.6)	31.7 (13.9-49.5)	30.8 (25.3-36.4)	47.5 (0-97.2)	44.8 (33.0-56.5)
Median OS (months, 95% CI)	11.8 (5.1-8.5)	10.5 (9.5-11.6)	64.8 (47.4-82.2)	59.1 (51.0-67.2)	103.1 (-)	75.4 (69.3-81.4)
Alive at last follow-up	0	3 (1.3%)	8 (34.8%)	9 (20.5%)	8 (61.5%)	7 (35.0%)
KPS at diagnosis						
90-100	6 (54.5%)	91 (40.4%)	7 (30.4%)	18 (46.3%)	5 (38.5%)	8 (44.4%)
70-80	3 (27.3%)	110 (48.9%)	14 (60.9%)	19 (43.9%)	7 (53.8%)	9 (50.0%)
<70	2 (18.2%)	24 (10.7%)	2 (8.7%)	4 (9.8%)	1 (7.7%)	1 (5.6%)
No data	-	4	-	3	-	2
Tumor location						
Frontal	4 (36.4%)	52 (22.8%)	9 (39.1%)	8 (18.2%)	5 (38.5%)	3 (15.0%)
Temporal	1 (9.1%)	64 (28.1%)	1 (4.3%)	13 (29.5%)	-	6 (30.0%)

Parietal	3 (27.3%)	27 (11.8%)	1 (4.3%)	8 (18.2%)	1 (7.7%)	5 (25.0%)
Occipital	-	11 (4.8%)	1 (4.3%)	-	-	-
Not localized to one site	3 (27.3%)	55 (24.1%)	9 (39.1%)	11 (25.0%)	5 (38.5%)	4 (20.0%)
Multifocal	-	3 (1.3%)	-	1 (2.3%)	-	1 (5.0%)
Others	-	16 (7.0%)	2 (8.7%)	3 (6.8%)	2 (15.4%)	1 (5.0%)
No data	-	1	-	-	-	-
Surgery						
Gross total resection	6 (54.5%)	95 (42.0%)	10 (45.5%)	22 (53.7%)	7 (58.8%)	9 (47.4%)
Subtotal resection (50-99%)	2 (18.2%)	85 (37.6%)	7 (31.8%)	13 (31.7%)	4 (30.8%)	8 (42.1%)
Partial resection (<50%)	3 (27.3%)	22 (9.7%)	4 (18.2%)	4 (9.8%)	2 (15.4%)	1 (5.3%)
Biopsy	-	24 (10.6%)	1 (4.5%)	2 (4.9%)	-	1 (5.3%)
No data	-	3	1	3	-	1
Review diagnosis						
Glioblastoma	11 (100.0%)	215 (93.9%)	23 (100.0%)	39 (88.6%)	13 (100.0%)	19 (95.0%)
Gliosarcoma	-	7 (3.1%)	-	2 (4.5%)	-	1 (5.0%)
Giant cell glioblastoma	-	7 (3.1%)	-	3 (6.8%)	-	-
First-line therapy						
RT alone	2 (18.2%)	58 (25.3%)	9 (39.1%)	10 (22.7%)	4 (30.8%)	1 (5.0%)
RT plus TMZ	8 (72.7%)	132 (57.6%)	10 (43.5%)	25 (56.8%)	7 (53.8%)	14 (70.0%)
RT plus nitrosourea	-	2 (0.9%)	2 (8.7%)	9 (20.5%)	1 (7.7%)	5 (25.0%)
Procarbazine plus lomustine alone	-	-	1 (4.3%)	-	-	-
RT plus PC	-	1 (0.4%)	-	-	-	-
TMZ alone	-	9 (3.9%)	-	-	-	-
Nitrosourea alone	1 (9.1%)	-	-	-	-	-
No therapy	-	27 (11.8%)	1 (4.3%)	-	1 (7.7%)	-
Salvage therapies						
Surgery (1)	2 (18.2%)	50 (21.8%)	4 (17.4%)	12 (27.3%)	-	7 (35.0%)
Surgery (2)	1 (9.1%)	9 (3.9%)	5 (21.7%)	2 (4.5%)	3 (23.1%)	1 (5.0%)
Surgery (>2)	-	1 (0.4%)	-	5 (13.9%)	-	3 (15.1%)
RT (first)	1 (9.1%)	3 (1.3%)	2 (8.7%)	-	1 (7.7%)	-
RT (reirradiation)	1 (9.1%)	17 (7.4%)	3 (13.0%)	8 (18.2%)	1 (7.7%)	4 (20.0%)
Chemotherapy (1)	3 (27.3%)	47 (20.5%)	8 (34.8%)	13 (29.5%)	5 (38.5%)	9 (45.0%)
Chemotherapy (2)	2 (18.2%)	23 (10.0%)	3 (13.0%)	8 (18.2%)	1 (7.7%)	3 (15.0%)

Chemotherapy (3)	-	5 (2.2%)	-	5 (11.4%)	-	-
Chemotherapy (>3)	-	1 (0.4%)	1 (4.3%)	3 (6.8%)	1 (7.7%)	1 (5.0%)
Other med. therapies (1)	1 (9.1%)	18 (7.9%)	1 (4.3%)	6 (13.6%)	1 (7.7%)	1 (5.0%)
Other med. therapies (>1)	-	3 (1.3%)	-	1 (2.3%)	-	-
None	5 (45.5%)	127 (55.5%)	8 (34.8%)	13 (29.5%)	6 (46.2%)	7 (35.0%)
MGMT promoter methylation status						
Methylated	4 (36.4%)	76 (33.8%)	17 (73.9%)	24 (54.5%)	10 (76.9%)	12 (59.1%)
Weakly methylated	1 (9.1%)	13 (5.8%)	4 (17.4%)	11 (25.0%)	2 (15.4%)	5 (22.7%)
Unmethylated	6 (54.5%)	136 (60.4%)	2 (8.7%)	9 (20.5%)	1 (7.7%)	3 (18.2%)
1p/19q codeletion						
Yes	2 (20.0%)	18 (8.4%)	4 (19.0%)	1 (2.6%)	2 (16.7%)	-
No	8 (80.0%)	196 (91.6%)	17 (81.0%)	38 (97.4%)	10 (83.3%)	19 (100.0%)
No data	1	15	2	5	1	1
EGFR amplification						
Yes	1 (9.1%)	102 (45.5%)	1 (4.3%)	19 (43.2%)	-	7 (35.0%)
No	10 (90.9%)	122 (54.5%)	22 (95.7%)	25 (56.8%)	13 (100.0%)	13 (65.0%)
TP53 mutation						
Yes	4 (40.0%)	32 (14.5%)	7 (30.4%)	7 (17.5%)	2 (15.4%)	2 (10.5%)
No	6 (60.0%)	189 (85.5%)	16 (69.6%)	33 (82.5%)	11 (84.6%)	17 (89.5%)
No data	1	8		4		1

Figure legend

Figure 1. Relative frequency of molecular marker aberrations by cohort: *IDH1/2* mutation status, *MGMT* promoter methylation status, *TP53* mutation status or *EGFR* amplification status in control (A), LTS-36 (B) and LTS-60 (C) patients.

Figure 2. Survival by molecular marker status in the LTS-36 cohort. OS is shown for the LTS-36 patients (left) and compared with the control cohort (right) stratified by *IDH1/2* mutation status (A,E), *MGMT* promoter methylation status (B,F), *TP53* mutation status (C,G) or *EGFR* amplification status (D,H).

Figure 3. Distribution of glioblastomas by *IDH1/2* mutation and *MGMT* promoter methylation status among the three patient groups: control (A), LTS-36 (B) and LTS-60 (C) patients.

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Supplementary Table 1. Individual profiles of LTS-36 patients with *IDH1/2*-mutant glioblastomas.

No	Age	Gender	<i>MGMT</i> promoter methylation	1p/19q codeletion	<i>EGFR</i> amplification	<i>TP53</i> mutation
1	36	male	methylyated	no	no	no
2	50	male	methylyated	yes	yes	yes
3	39	female	methylyated	no	no	no
4	35	female	methylyated	no	no	no
5	41	male	methylyated	no	no	yes
6	37	male	methylyated	n.a.	no	no
7	44	female	methylyated	no	no	no
8	24	male	methylyated	no	no	no
9	71	female	methylyated	no	no	no
10	48	female	methylyated	yes	no	no
11	54	male	weakly methylyated	no	no	no
12	50	female	methylyated	no	no	no
13	44	male	unmethylyated	no	no	no
14	45	female	methylyated	no	no	no
15	55	female	methylyated	no	no	yes
16	29	female	weakly methylyated	no	no	yes
17	39	female	methylyated	yes	no	no
18	22	male	methylyated	no	no	yes
19	24	female	unmethylyated	no	no	yes
20	45	male	methylyated	yes	no	no
21	55	male	weakly methylyated	no	no	no
22	38	male	methylyated	n.a.	no	yes
23	35	male	weakly methylyated	no	no	no

Supplementary Table 2. Individual profiles of LTS-36 patients with *IDH1/2*-wildtype glioblastomas.

No	Age	Gender	<i>MGMT</i> promoter methylation	1p/19q codeletion	<i>EGFR</i> amplification	<i>TP53</i> mutation
1	60	female	methyalted	no	no	no
2	57	male	weakly methyalted	no	no	n.a.
3	52	female	methyalted	no	yes	no
4	56	female	methyalted	no	yes	no
5	63	female	methyalted	no	yes	no
6	25	female	methyalted	no	no	yes
7	49	female	weakly methyalted	n.a.	no	no
8	71	male	methyalted	no	no	no
9	56	female	weakly methyalted	no	yes	no
10	66	male	weakly methyalted	n.a.	yes	n.a.
11	56	male	methyalted	no	yes	no
12	40	female	weakly methyalted	no	no	no
13	50	male	weakly methyalted	no	yes	no
14	32	female	methyalted	no	no	yes
15	51	male	unmethyalted	no	no	no
16	62	male	weakly methyalted	no	no	no
17	74	female	unmethyalted	no	yes	no
18	39	female	methyalted	no	no	no
19	36	female	methyalted	no	no	no
20	57	male	methyalted	no	no	no
21	41	male	methyalted	no	no	no
22	60	female	methyalted	no	yes	no
23	68	male	methyalted	no	yes	no
24	52	male	methyalted	no	yes	yes
25	55	female	weakly methyalted	no	no	no
26	48	male	methyalted	no	yes	no
27	56	female	methyalted	no	yes	no
28	49	female	unmethyalted	yes	no	yes
29	48	male	methyalted	no	yes	no
30	44	male	unmethyalted	no	no	no
31	59	male	methyalted	no	no	no
32	60	male	weakly methyalted	no	yes	no
33	65	male	unmethyalted	no	yes	no
34	43	male	methyalted	no	no	no
35	64	female	weakly methyalted	no	no	yes
36	42	male	weakly methyalted	n.a.	no	yes
37	42	female	methyalted	no	yes	n.a.
38	62	male	methyalted	no	yes	no
39	60	female	methyalted	n.a.	yes	n.a.
40	31	female	unmethyalted	no	no	no
41	60	male	methyalted	no	no	no
42	21	female	unmethyalted	no	no	no

43	29	male	methylated	no	no	no
44	59	male	unmethylated	n.a.	no	yes

Figure 1

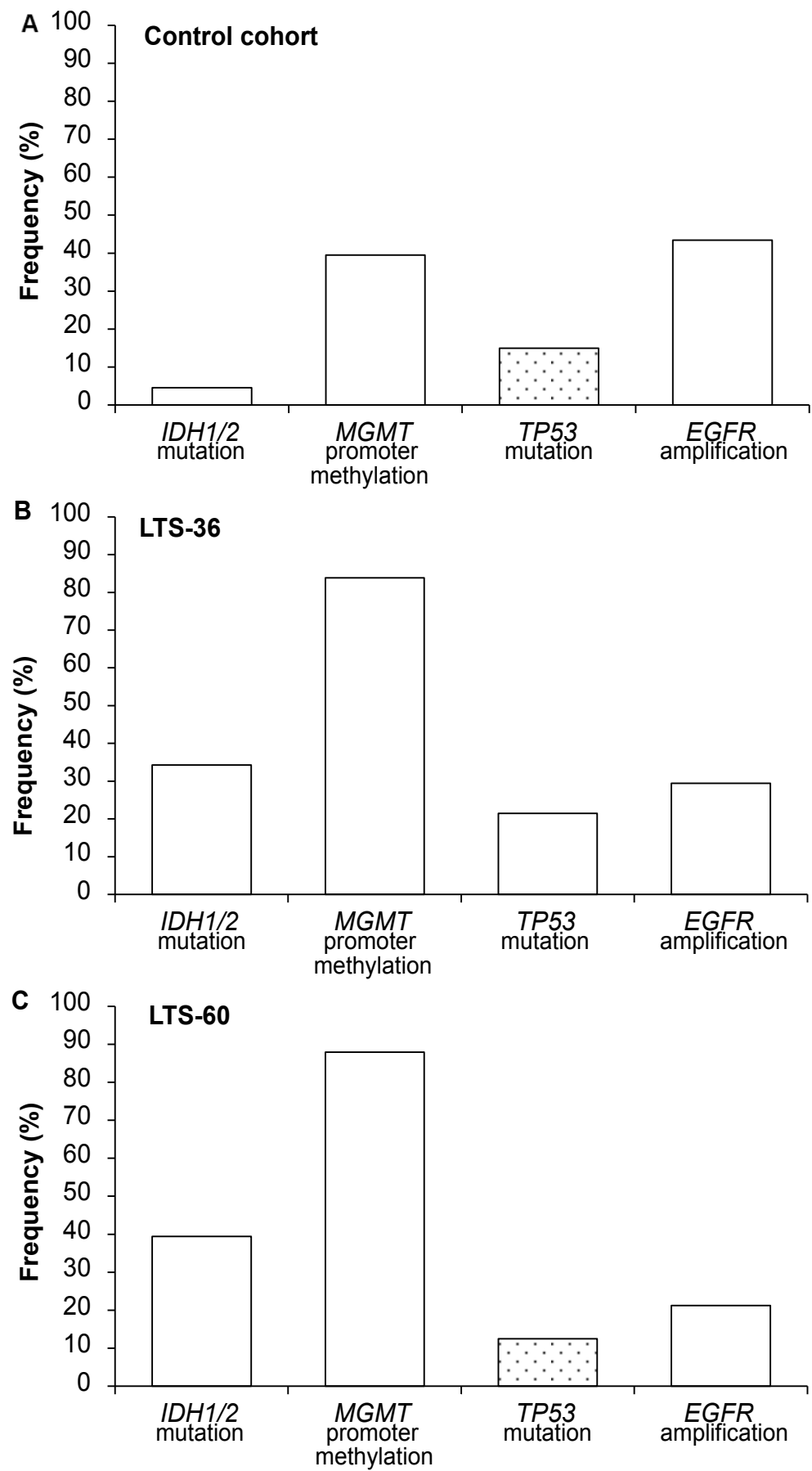


Figure 2

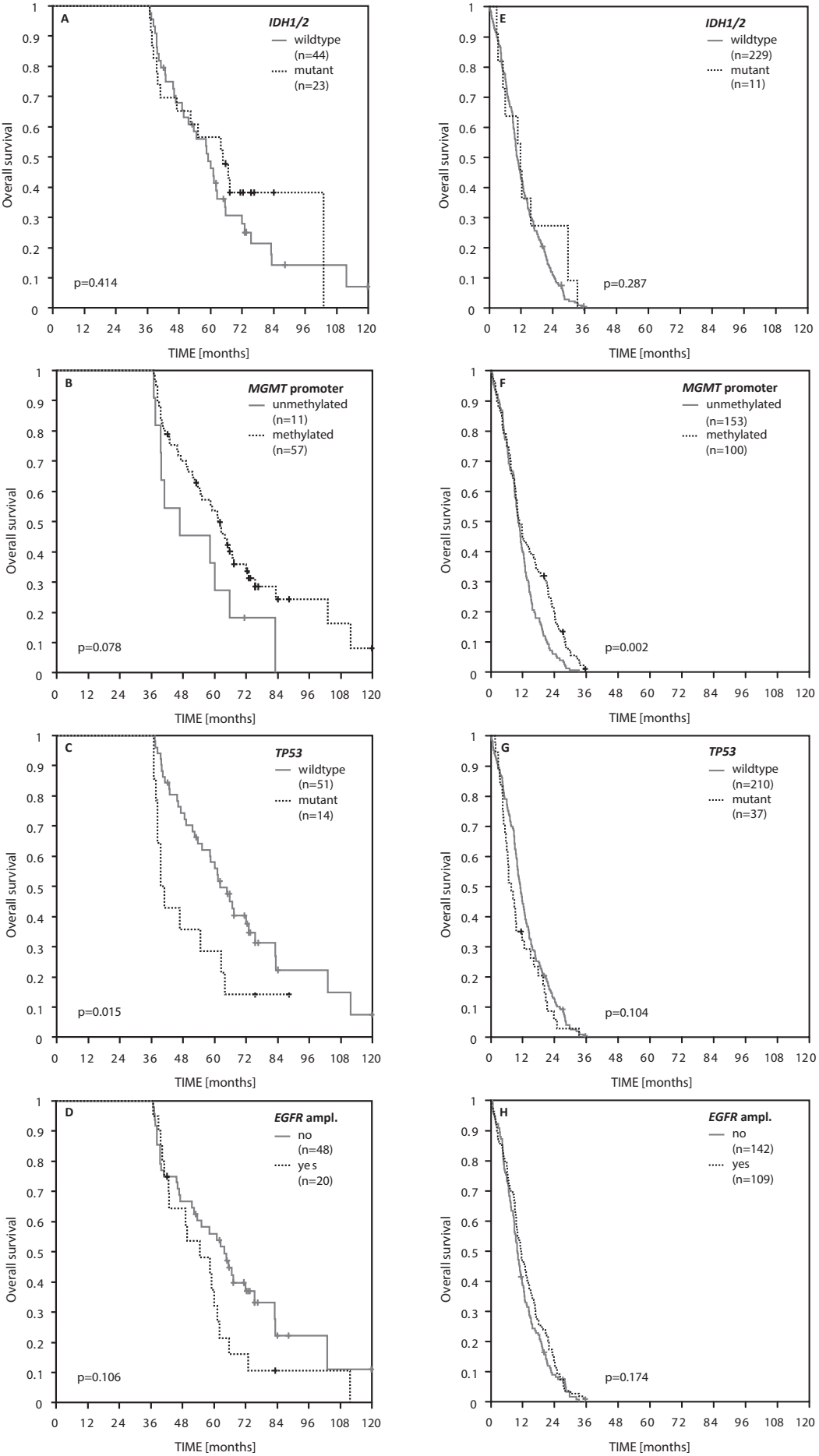


Figure 3

